ATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCAGCTCCGC TCGTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGC TGGAGTCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCA CCCTCAACCCGCTGAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCA CCTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCTGGGTCCCCAGGCCGTG GGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGGCCCTGACAGTGTTTGGC

FIG 1A

 ${\tt CGTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCT}$ GGAGTCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCAC CCTCAACCCGCTGAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCAC CTCATAGAGGGCTCCCAGAAGTGTGTGGCTGAGCTGGGTCCCCAGGCCGTGG GGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTGACAGTGTTTGGC

FIG. 1B

TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTGGAGTC GGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAAC CCGCTGAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAG AGGGCTCCCAGAAGTGTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGT GAAGGCCCTGAAGGCCCTGCTGGGGGCCCTGACAGTGTTTGGC

FIG. 1C

MKLAALLGLCVALSCSSARAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTL NPLKLLLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG

FIG. 2A

RAFLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHLIEGSQKCVAELGPQAVGAVKALKALLGALTVFG FIG. 2B

FLVGSAKPVAQPVAALESAAEAGAGTLANPLGTLNPLKLLLSSLGIPVNHLIEGS QKCVAELGPQAVGAVKALKALLGALTVFG FIG. 2C ATGAAGCTTACCACCACCTTTCTAGTGCTCTGTGTGGCTCTGCTCAGTGACTC TGGTGTTGCTTTCATGGACTCATTGGCCAAGCCTGCGGTAGAACCCGTGG CCGCCCTTGCTCCAGCTGCAGAGGCTGTGGCAGGGGCTGTGCCTAGCCTACC ATTAAGCCACTTGGCCATCCTGAGGTTCATCCTGGCCAGCATGGGCATCCCAT TGGATCCTCTCATAGAGGGATCCAGGAAGTGTGTCACCGAGCTGGGCCCTGA GGCTGTAGGAGCTGTGAAGTCACTGCTGGGGGTCCTGACAATGTTCGGT

FIG. 3A

 ${\tt GTTGCTTTCATGGACTCATTGGCCAAGCCTGCGGTAGAACCCGTGGCCGC}$ CCTTGCTCCAGCTGCAGAGGCTGTGGCAGGGGCTGTGCCTAGCCTACCATTA AGCCACTTGGCCATCCTGAGGTTCATCCTGGCCAGCATGGGCATCCCATTGG ATCCTCTCATAGAGGGATCCAGGAAGTGTGTCACCGAGCTGGGCCCTGAGGC TGTAGGAGCTGTGAAGTCACTGCTGGGGGTCCTGACAATGTTCGGT

FIG. 3B

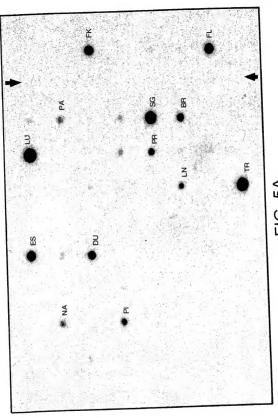
TTCTTCATGGACTCATTGGCCAAGCCTGCGGTAGAACCCGTGGCCGCCCTTGC TCCAGCTGCAGAGGCTGTGGCAGGGGCTGTGCCTAGCCTACCATTAAGCCAC TTGGCCATCCTGAGGTTCATCCTGGCCAGCATGGGCATCCCATTGGATCCTCT CATAGAGGGATCCAGGAAGTGTGTCACCGAGCTGGGCCCTGAGGCTGTAGGA GCTGTGAAGTCACTGCTGGGGGTCCTGACAATGTTCGGT FIG. 3C

MKLTTIFLVLCVALLSDSGVAFFMDSLAKPAVEPVAALAPAAEAVAGAVPSLPLSHLAILRFILASMGIPLDPLIEGSRKCVTELGPEAVGAVKSLLGVLTMFG

FIG. 4A

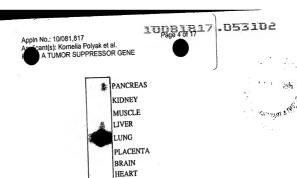
VAFFMDSLAKPAVEPVAALAPAAEAVAGAVPSLPLSHLAILRFILASMGIPLDPLI EGSRKCVTELGPEAVGAVKSLLGVLTMFG FIG. 4B

SRKCVTELGPEAVGAVKSLLGVLTMFG FIG. 4C



The case of

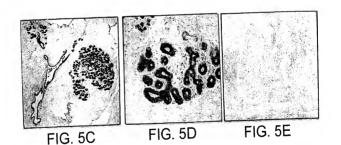
FIG. 5A

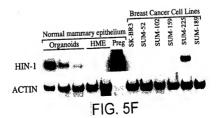


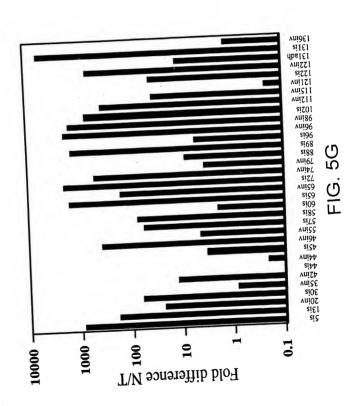
PROSTATE
THYMUS
SPLEEN

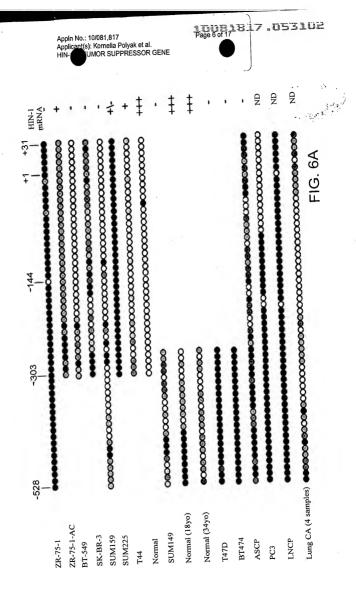
PBL COLON SM. INTESTINE OVARY TESTIS

FIG. 5B









ZR75-1 N MU MU FIG. 6B Medium MCF10A SUM159 G H RT474 ZR75-1 SUM159 SUM225 Cells MCF10A H SUM159 MEDIUM H BT549 293 cells 5aza-C ACTIN HIN-1 CELLS H The same of the sa

CGGCCGGGGAGGCGGCCGGGAGTGAGGCCTGATCGTCCCTGGCGCCTCCACC TCCCCAGGCGCAGAAGGCGCCCACGAGGACCCCCCAGTGCCCGACGTTGCCAC GGTCTGGGATCAGAGGCAGGGACCAGGAGCAGGAACTGCGCCCCCCG CCCCTGCCCTGGCGCGAGGGAAGCTCCCTCACCNGAGGGAAGCTCCCCTCAC CCGGCCCAGCCCTGCAGGGGGGGCGCGTGGGGTCAGACCGCAAAGCGAAGGT GGGCCCCAGCGCCTGCCAAGAGGAAGTCCTCGAGGCCCGGGCAGGGAAGGG GGCACGGGCTTCCCAGGGCCCGCCGGCCGCAGCAGGAAGTTGGCCAGGGCA CGGCCGTGAGCGGAGCGGGCAGGCCTTTCTCAGGAGCGCGGGCGAGGCCGG CGCTGGAGGGCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGC AGCCGCAGGTTCCCCGCGCGCCCCGAGCCCCCGCGCC FIG 8

GTTCTCTGTTTTGTTGGTAGGCGTTGCTTTCTTGGTGGATTCACTGGCCAAG CCTGTGGTAGAACCCGTGGCTGCCATTGCTACAGCTGCAGAGGCTGTGGCAG GGGCTGTGCCTAGCCTACCATTAAGCCACTTGGCCATCCTGAGGTTCATCGTG ACCAGCCTGGGCATCCCATTGGATCCTCTCATAGATGGTTCCAGGAAGTGCGT CACCGAGCTGGGCCCTGAGGCTGTAGGAGCTGTGAAGTCACTGCTGGGGGCC FIG. 9A CTGACAACGTTCGGT

VLCFVLVGVAFLVDSLAKPVVEPVAAIATAAEAV AGAVPSLPLSHLAILRFIVTSL GIPLDPLIDGSRKCVTELGPEAVGAVKSLLGALTTFG FIG. 9B

TTCTTGGTGGATTCACTGGCCAAGCCTGTGGTAGAACCCGTGGCTGCCATTGCCATTGCCATTGCCATTGCCCCATTGCCATTGCCCATTGCCATTGCCATTGCCATTGCCATTGCCATTGCCCATTGCATTGCATTGCATTGCCATTGCCATTGCCATTGCCATTGCCATTGCATTACAGCTGCAGAGGCTGTGGCAGGGGCTGTGCCTAGCCTACCATTAAGCCAC TTGGCCATCCTGAGGTTCATCGTGACCAGCCTGGGCATCCCATTGGATCCTCT CATAGATGGTTCCAGGAAGTGCGTCACCGAGCTGGGCCCTGAGGCTGTAGGA GCTGTGAAGTCACTGCTGGGGGCCCTGACAACGTTCGGT FIG. 9C

LL EAVAGAVP VNHLI GIPUDPUL GIPLDPLI RAFLVG VAFFMD ⋖ > TL 4 GA 14 SSARAFEDSGVAFF GAG 1 4 EGSOKCVAELGPOAVGAVKA EGSRKCVTELGPEAVGAVKS DGSRKCVTELGPEAVGAVKS I D K . ш S SMS 1 4 သင Ü PULSHLALLS LPLSHLALLEFT VA LPLSHLALERFIVT LPLSHLALLEFT V S 4 ۲ H S AALAP VAAI Ы S , > LLGLCVAL QPVAAL > A u > VEC U \_1 P V A Q P
P A V E P
P V V E P а > . -4 H A K 1 A K 1 A K 1 M < F MKL MKL SL S Human HIN1 Human HIN1 Mouse HIN1 Human HIN1 Mouse HIN1 Human HINI Mouse HIN1 Rat HIN-1 Rat HIN-1 Rat HIN-1

N

11

۵

> C

4

S

123

**ტ** ი

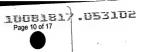
Mouse HIN1

Rat HIN-1

LL

ក្ **9** 5 Σ > G A L G V L G A L G A L Human HIN1 Mouse HIN1 Rat HIN-1

Appln No.: 10/081,817 Applicant(s): Kornelia Polyak et al. A TUMOR SUPPRESSOR GENE



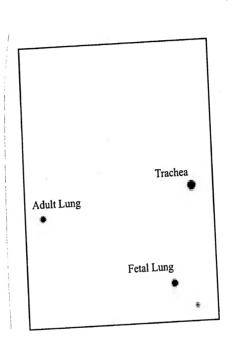
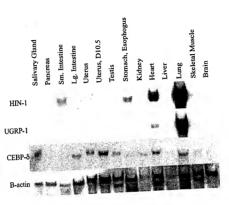
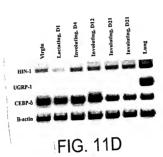


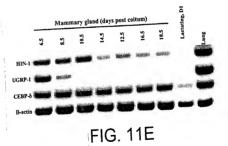
FIG. 11A



## FIG. 11B

## Whole Embryo, d.p.c. Whole Embryo, d.p.c. 9 8 8 8 18.5 1 10 8 19 10 18 1 10 19 10 19 1 10 19 1 10 1





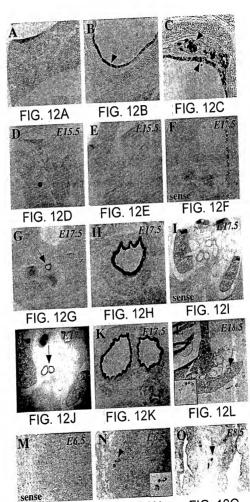
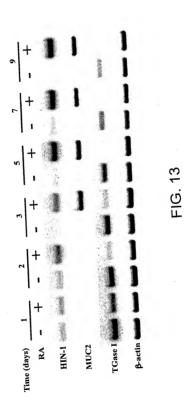


FIG. 12M FIG. 12N FIG. 12O

Appln No.: 10/081,817
Applicant(s): Kornelia Polyak et al.
1, A TUMOR SUPPRESSOR GENE

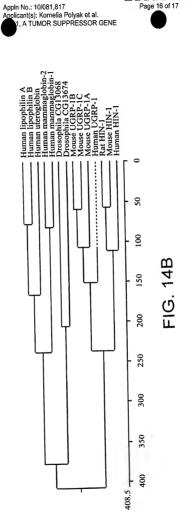


Appln No.: 10/081,817 Applicant(s): Kornelia Polyak et al. HIN-1, A TUMOR SUPPRESSOR GENE

ENE

A Y T ELGPERASE RIGPORGA AVTAPVARA AATAPVARA FIG. 14A 1 4 8 8 0 0 4 0 0 VPLPV AAAAPV APAA BELVE BELVE BELTE BAAKE AAKE SARAFE SABPKPA VAPEA M Z K K 0 4 4 A N (0 (0) X PUNKLLIK TOOT PUKLLUSSLOT AAPVVAAAKTA 4 4 4 ב ט ט ב 10>4 F 1 2 F 7 0 Z 4 4 X 1 > 4 4 00 > P H D W O Z H D C C N \* 4 K H XX K K W M × Human UGRP-1 Human HIN-1 Drosophila CG13068 Drosophila CG13674 Human HIN-1 Drosophila CG13068 Drosophila CG13674 Human HIN-1 Drosophila CG13068 Drosophila CG13674 Human UGRP-1 Human UGRP-1

the state of the s



Appin No.: 10/081,817 Applicant(s): Kornelia Polyak et al. IIN-1, A TUMOR SUPPRESSOR GENE Page 17 of 17

GCTGAGCCCAAGCCCGCTATCCTGGCCGCCGCTCCAGTGGTTGCAGCTGCTCC TGCCGGCGTGGTCACCGCTACCAGTTCGCAGTACGTGGCCCGCAACTTCAAC GGTGTGGCTGCTCCAGTTGTTGCCGCTGCCTACACCGCTCCAGTTGCCGC CGCTGCCTATACCGCTCCAGTTGCCGCCGCTGCTTATACCGCTCCAGTTGCCG CTGCCTACTCTGCTTATCCGTATGCCGCCTACCCTTACAGCGCTGCATACACC ACTGTTTTG

FIG. 15

ATGAAATTCCTCGCCGTCTGCTTCTTCGCTGTTGTGGCTGTGGCTGCCAA ACCCGGTATTGTGGCTCCTCTGGCCTACACCGCTCCGGCTGTGGTGGGCAGTG CCGCCTACGTGGCTCCCTACGCCTCCAGCTACACCGCCAACTCGGTGGCCCAC AGCGCCGCCTTCCCAGCTGCCTACACCGCCGCCTACACTGCTCCCGTTGCTGC TGCCTATACCGCTCCAGTGGCTGCTGCTTATACCGCTCCAGTGGCCGCTGCGT ACGCCGCCCCAGCTGCCTATACCGCTGCCTACACCGCCCCCATTGCCCGTTAT GCCGCCACCCCTTCGCAGCACCCATCGCCGCTCCCGTGGCTGCCGCCTACAC CGCCCCATCGCCGCCGCTGCCCCAGTTCTGCTGAAGAAG

FIG. 16